F56L, F56T or F56G; (b) N55Q, N55R, N55K, N55S, N55G, N55A or N55T; (c) Y51L, Y51V, Y51A, Y51N, Y51Q, Y51S or Y51G; (d) T150I; (e) S54P; and (f) S57P.

79. The method of claim **78**, wherein the variant comprises any of the combinations of mutations/substitutions selected from the group consisting of: (i) one or more mutations at the following positions N40, D43, E44, S54, S57, Q62, R97, E101, E124, E131, R142, T150 and R192; (ii) mutations at Y51/N55, Y51/F56, N55/F56 or Y51/N55/F56; (iii) Q42R or Q42K; (iv) K49R; (v) N102R, N102F, N102Y or N102W; (vi) D149N, D149Q or D149R; (vii) E185N, E185Q or E185R; (viii) D195N, D195Q or D195R; (ix) E201N, E201Q or E201R; (x) E203N, E203Q or E203R; and (xi) deletion of one or more of the following positions F48, K49, P50, Y51, P52, A53, S54, N55, F56 and S57.

80. The method of claim **77**, wherein the target analyte is a target polynucleotide and step (a) further comprises contacting the polynucleotide with a polynucleotide binding protein such that the protein controls the movement of the polynucleotide through the pore.

81. The method of claim **80**, wherein the polynucleotide binding protein is a helicase or is derived from a helicase.

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